

## SEQUENCE LISTING

&lt;110&gt; BASF AKTIENGESELLSCHAFT et al.

<120> METHODS FOR THE PREPARATION OF A FINE  
CHEMICAL BY FERMENTATION

&lt;130&gt; BGI-159PC2

&lt;150&gt; PCT/IB2003/006464

&lt;151&gt; 2003-12-18

&lt;160&gt; 15

&lt;170&gt; FastSEQ for Windows Version 4.0

&lt;210&gt; 1

&lt;211&gt; 1650

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)...(1627)

&lt;400&gt; 1

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Ala Asn Ala Tyr Val Ala Ala Ile Asp Gln Gly Thr Thr Ser Thr Arg
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Cys Ile Phe Ile Asp Ala Gln Gly Lys Val Val Ser Ser Ala Ser Lys
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Glu His Arg Gln Ile Phe Pro Gln Gln Gly Trp Val Glu His Asp Pro
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Glu Glu Ile Trp Asp Asn Ile Arg Ser Val Val Ser Gln Ala Met Val
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tcc att gac atc acc cca cac gag gtt gca tcg ctg gga gtc acc aac 355
Ser Ile Asp Ile Thr Pro His Glu Val Ala Ser Leu Gly Val Thr Asn
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cag cgc gaa acc acc gtg gtg tgg gac aag cac acc ggc gaa cct gtc 403
Gln Arg Glu Thr Thr Val Val Trp Asp Lys His Thr Gly Glu Pro Val
                               90       95       100

tac aac gca atc gtg tgg caa gac acc cgc acc tct gac att tgc cta 451
Tyr Asn Ala Ile Val Trp Gln Asp Thr Arg Thr Ser Asp Ile Cys Leu
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| Glu Ile Ala Gly Glu Glu Gly Gln Glu Lys Trp Leu Asp Arg Thr Gly |      |
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| ctg ctg atc aac tcc tac cca tgc ggg ccc aaa atc aag tgg att ctc | 547  |
| Leu Leu Ile Asn Ser Tyr Pro Ser Gly Pro Lys Ile Lys Trp Ile Leu |      |
| 135 140 145   |      |
| gac aac gtt gag gga gct cgc gaa cgc gcc gaa aag ggc gac ctt ttg | 595  |
| Asp Asn Val Glu Gly Ala Arg Glu Arg Ala Glu Lys Gly Asp Leu Leu |      |
| 150 155 160 165   |      |
| ttt ggc acc atg gat acc tgg gtg ctg tgg aac ctg acc ggc ggt gtc | 643  |
| Phe Gly Thr Met Asp Thr Trp Val Leu Trp Asn Leu Thr Gly Gly Val |      |
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| cgc ggc gac gac ggt gat gat gcc atc cac gtc acc gat gtc acc aac | 691  |
| Arg Gly Asp Asp Gly Asp Asp Ala Ile His Val Thr Asp Val Thr Asn |      |
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| gca tcc cgc aca cta ttg atg gat ctc cgc acg caa cag tgg gat cca | 739  |
| Ala Ser Arg Thr Leu Leu Met Asp Leu Arg Thr Gln Gln Trp Asp Pro |      |
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| gaa cta tgc gaa gcc cta gac att ccg atg tcc atg ctc cct gag att | 787  |
| Glu Leu Cys Glu Ala Leu Asp Ile Pro Met Ser Met Leu Pro Glu Ile |      |
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| cgt ccc tcc gtc gga gaa ttc cgc tcc gtg cgc cac cgc gga acc cta | 835  |
| Arg Pro Ser Val Gly Glu Phe Arg Ser Val Arg His Arg Gly Thr Leu |      |
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| gcc gac gtc ccg att act ggc gtg ctc ggc gac cag caa gcg gcc ctt | 883  |
| Ala Asp Val Pro Ile Thr Gly Val Leu Gly Asp Gln Gln Ala Ala Leu |      |
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| ttt ggt cag ggc gga ttc cac gaa ggt gct gct aaa aat acc tac ggc | 931  |
| Phe Gly Gln Gly Gly Phe His Glu Gly Ala Ala Lys Asn Thr Tyr Gly |      |
| 265 270 275   |      |
| acc ggc ctc ttc ctg ctg atg aac acc ggc acc tgc ttg aag att tcc | 979  |
| Thr Gly Leu Phe Leu Leu Met Asn Thr Gly Thr Ser Leu Lys Ile Ser |      |
| 280 285 290   |      |
| gag cac ggc ctg ctg tcc acc atc gcc tat caa cgg gaa gga tcc gct | 1027 |
| Glu His Gly Leu Leu Ser Thr Ile Ala Tyr Gln Arg Glu Gly Ser Ala |      |
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| Pro Val Tyr Ala Leu Glu Gly Ser Val Ser Met Gly Gly Ser Leu Val |      |
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| cag tgg ctg cgc gac aac cta cag cta atc ccc aac gca cca gcg att | 1123 |
| Gln Trp Leu Arg Asp Asn Leu Gln Leu Ile Pro Asn Ala Pro Ala Ile |      |
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| gaa aac ctc gcc cga gaa gtc gaa gac aac ggt ggc gtt cat gtt gtc | 1171 |
| Glu Asn Leu Ala Arg Glu Val Glu Asp Asn Gly Gly Val His Val Val |      |
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| cca gca ttc acc gga ctg ttc gca cca cgt tgg cgc ccc gat gct cgt | 1219 |

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 360 365 370

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 375 380 385

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 Gly Val Ala Phe Ala Ala Gly Leu Gly Ser Gly Phe Phe Lys Thr Thr  
 455 460 465

gac gag atc gaa aaa ctt att gca gtg aag aaa gtc tgg aac cct gac 1555  
 Asp Glu Ile Glu Lys Leu Ile Ala Val Lys Lys Val Trp Asn Pro Asp  
 470 475 480 485

atg agc gaa gaa gag cgc gaa cgt cgc tat gcc gaa tgg aat agg gca 1603  
 Met Ser Glu Glu Glu Arg Glu Arg Arg Tyr Ala Glu Trp Asn Arg Ala  
 490 495 500

gtg gag cat tct tat gac cag gcc tagctgattt gggtcggcct tta 1650  
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&lt;210&gt; 2

&lt;211&gt; 509

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 2

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 20 25 30  
 Ser Ser Ala Ser Lys Glu His Arg Gln Ile Phe Pro Gln Gln Gly Trp  
 35 40 45  
 Val Glu His Asp Pro Glu Glu Ile Trp Asp Asn Ile Arg Ser Val Val  
 50 55 60  
 Ser Gln Ala Met Val Ser Ile Asp Ile Thr Pro His Glu Val Ala Ser  
 65 70 75 80  
 Leu Gly Val Thr Asn Gln Arg Glu Thr Thr Val Val Trp Asp Lys His  
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 Thr Gly Glu Pro Val Tyr Asn Ala Ile Val Trp Gln Asp Thr Arg Thr  
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| Leu Asp Arg Thr Gly   | Leu Leu Ile Asn Ser Tyr Pro Ser Gly Pro Lys |     |
| 130   | 135   | 140 |
| Ile Lys Trp Ile Leu Asp Asn Val Glu Gly Ala Arg Glu Arg Ala Glu |   |     |
| 145   | 150   | 155 |
| Lys Gly Asp Leu Leu Phe Gly Thr Met Asp Thr Trp Val Leu Trp Asn |   |     |
| 165   | 170   | 175 |
| Leu Thr Gly Gly Val Arg Gly Asp Asp Gly Asp Asp Ala Ile His Val |   |     |
| 180   | 185   | 190 |
| Thr Asp Val Thr Asn Ala Ser Arg Thr Leu Leu Met Asp Leu Arg Thr |   |     |
| 195   | 200   | 205 |
| Gln Gln Trp Asp Pro Glu Leu Cys Glu Ala Leu Asp Ile Pro Met Ser |   |     |
| 210   | 215   | 220 |
| Met Leu Pro Glu Ile Arg Pro Ser Val Gly Glu Phe Arg Ser Val Arg |   |     |
| 225   | 230   | 235 |
| His Arg Gly Thr Leu Ala Asp Val Pro Ile Thr Gly Val Leu Gly Asp |   |     |
| 245   | 250   | 255 |
| Gln Gln Ala Ala Leu Phe Gly Gln Gly Gly Phe His Glu Gly Ala Ala |   |     |
| 260   | 265   | 270 |
| Lys Asn Thr Tyr Gly Thr Gly Leu Phe Leu Leu Met Asn Thr Gly Thr |   |     |
| 275   | 280   | 285 |
| Ser Leu Lys Ile Ser Glu His Gly Leu Leu Ser Thr Ile Ala Tyr Gln |   |     |
| 290   | 295   | 300 |
| Arg Glu Gly Ser Ala Pro Val Tyr Ala Leu Glu Gly Ser Val Ser Met |   |     |
| 305   | 310   | 315 |
| Gly Gly Ser Leu Val Gln Trp Leu Arg Asp Asn Leu Gln Leu Ile Pro |   |     |
| 325   | 330   | 335 |
| Asn Ala Pro Ala Ile Glu Asn Leu Ala Arg Glu Val Glu Asp Asn Gly |   |     |
| 340   | 345   | 350 |
| Gly Val His Val Val Pro Ala Phe Thr Gly Leu Phe Ala Pro Arg Trp |   |     |
| 355   | 360   | 365 |
| Arg Pro Asp Ala Arg Gly Val Ile Thr Gly Leu Thr Arg Phe Ala Asn |   |     |
| 370   | 375   | 380 |
| Arg Lys His Ile Ala Arg Ala Val Leu Glu Ala Asn Ala Phe Gln Thr |   |     |
| 385   | 390   | 395 |
| Arg Glu Val Val Asp Ala Met Ala Lys Asp Ala Gly Lys Ala Leu Glu |   |     |
| 405   | 410   | 415 |
| Ser Leu Arg Val Asp Gly Ala Met Val Glu Asn Asp Leu Leu Met Gln |   |     |
| 420   | 425   | 430 |
| Met Gln Ala Asp Phe Leu Gly Ile Asp Val Gln Arg Leu Glu Asp Val |   |     |
| 435   | 440   | 445 |
| Glu Thr Thr Ala Val Gly Val Ala Phe Ala Ala Gly Leu Gly Ser Gly |   |     |
| 450   | 455   | 460 |
| Phe Phe Lys Thr Thr Asp Glu Ile Glu Lys Leu Ile Ala Val Lys Lys |   |     |
| 465   | 470   | 475 |
| Val Trp Asn Pro Asp Met Ser Glu Glu Glu Arg Glu Arg Arg Tyr Ala |   |     |
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| Glu Trp Asn Arg Ala Val Glu His Ser Tyr Asp Gln Ala             |   |     |
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&lt;211&gt; 35

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&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide

&lt;400&gt; 3

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35

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<220>  
 <223> Oligonucleotide

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34

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 <213> *Corynebacterium glutamicum*

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 tttaaatecgc tagcgggctg ctaaaggaag cggaacacgt agaaagccag tccgcagaaa 180  
 cgggtgctgac cccggatgaa tgtcagctac tgggctatct ggacaaggga aaacgcaagc 240  
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atc 4323

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&lt;210&gt; 6

&lt;211&gt; 5860

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 6

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| gccaagcttg  | catgcctgca  |             |             |             |             | 6680 |

&lt;210&gt; 15

&lt;211&gt; 6272

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 15

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| atggtgtctt | cccctgaggc | tggaaactcac | ggcctgtggg | gcgcaatcgg | tgacgcgtg  | 180 |
| gctcagcagg | gcgctgacct | tggccctctg  | ggacttccaa | ccagtaatga | atacaccgtt | 240 |
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| aggaggcggg | gttttctcca | atcaaaagcc  | aattaaaggc | cgacccaaat | cagctaggcc | 420 |



|             |             |             |             |             |             |      |
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